

Sequence alignment for 10/560,322

RESULT 1
US-09-850-948-2
; Sequence 2, Application US/09850948
; Patent No. 6919176
; GENERAL INFORMATION:
; APPLICANT: Yang, Jianxin
; APPLICANT: An, Songzhu
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer
; FILE REFERENCE: 018781-008300US
; CURRENT APPLICATION NUMBER: US/09/850,948
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor 4 (GPR4)
US-09-850-948-2

Result 2
US-10-267-811-2
; Sequence 2, Application US/10267811
; Publication No. US20030109044A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: METHODS OF USING 279, A HUMAN G
; TITLE OF INVENTION: PROTEIN-COUPLED PROTEIN RECEPTOR
; FILE REFERENCE: MPI01-227P1RM
; CURRENT APPLICATION NUMBER: US/10/267,811
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/329,648
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-267-811-2

Query Match 98.7%; Score 1907; DB 4; Length 362;
Best Local Similarity 98.9%; Pred. No. 5.1e-175;
Matches 358; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MGNHTWEGCHVDSRVDHLHPPSLYIFVIGVGLPTNCLALWAAYRQVQQQRNQLGVYLMNLS	60
Db	1	MGNHTWEGCHVDSRVDHLHPPSLYIFVIGVGLPTNCLALWAAYRQVQQQRNELGVYLMNLS	60
Qy	61	IADLLYICTLPLWVDYFLHHDNWIHGPGSCKLPGFIFYTNIYISIAFLCCISVDRYLAVA	120
Db	61	IADLLYICTLPLWVDYFLHHDNWIHGPGSCKLPGFIFYTNIYISIAFLCCISVDRYLAVA	120
Qy	121	HPLRFARLRRVKTAVAVSSVVWATELGANSAPLFHDELFRDYNHTFCFEKPMEGWVAW	180
Db	121	HPLRFARLRRVKTAVAVSSVVWATELGANSAPLFHDELFRDYNHTFCFEKPMEGWVAW	180
Qy	181	MNLYRVFVGFLFPWALMLLSYRGILRAVRGSVSTERQEAKIKRLALSLIAIVLVCFAPY	240
Db	181	MNLYRVFVGFLFPWALMLLSYRGILRAVRGSVSTERQEAKIKRLALSLIAIVLVCFAPY	240
Qy	241	HVLLLSRSAIYLGRPWDCGFEERVFSAYHSSLRAFTSLNCVADPILYCLVNEGARSDVAKA	300
Db	241	HVLLLSRSAIYLGRPWDCGFEERVFSAYHSSLRAFTSLNCVADPILYCLVNEGARSDVAKA	300
Qy	301	LHNLLRFLASDKPQEMANASLTLETPLTSKRNSTAKAMTGSWAATPPSEGDQVQLKMLPP	360
Db	301	LHNLLRFLASDKPQEMANASLTLETPLTSKRNSTAKAMTGSWAATPPSQGDQVQLKMLPP	360
Qy	361	AQ 362	
Db	361	AQ 36	

RESULT 3
A57641
G protein-coupled receptor 4 - human
C;Species: Homo sapiens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57641
R;Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.;
Tsilfidis, C.; Neville, C.E.; Narang, M.; Korneluk, R.G.
Genomics 30 84-88 1995

A;Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome 19q13.3.
A;Reference number: A57641; MUID:96129306; PMID:8595909
A;Accession: A57641
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-362 <MAH>
A;Cross-references: UNIPROT:P46093; UNIPARC:UPI0000050428; GB:U21051;
NID:g687793; PIDN:AAA98457.1; PID:g687794
C;Genetics:
A;Gene: GDB:GPR4
A;Cross-references: GDB:371710; OMIM:600551
A;Map position: 19q13.3-19q13.3
A;Introns: #status absent
C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor

Query Match 98.7%; Score 1907; DB 2; Length 362;
Best Local Similarity 98.9%; Pred. No. 1.6e-170;
Matches 358; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MGNHTWEGCHVDSRVDHLHPPSLYIFVIGVGLPTNCLALWAAYRQVQQRNQLGVYLMNLS	60
Db	1	MGNHTWEGCHVDSRVDHLFPPSLYIFVIGVGLPTNCLALWAAYRQVQQRNELGVYLMNLS	60
Qy	61	IADLLYICTLPLWVDYFLHHNDWIHGPGSCKLPGFIFYTNIYISIAFLCCISVDRYLAVA	120
Db	61	IADLLYICTLPLWVDYFLHHNDWIHGPGSCKLFGFIFYTNIYISIAFLCCISVDRYLAVA	120
Qy	121	HPLRFARLRRVKTAVAVSSVVWATELGANSAPLFHDELFRDYNHTFCFEKPMEGWVAW	180
Db	121	HPLRFARLRRVKTAVAVSSVVWATELGANSAPLFHDELFRDYNHTFCFEKPMEGWVAW	180
Qy	181	MNLYRVFVGFLFPWALMLLSYRGILRAVRGSVSTERQEAKIKRLALSLIAIVLVCFAPY	240
Db	181	MNLYRVFVGFLFPWALMLLSYRGILRAVRGSVSTERQEAKIKRLALSLIAIVLVCFAPY	240
Qy	241	HVLLLSRSAIYLGRPDCGFEERVFSAYHSSLRAFTSLNCVADPILYCLVNNEGARSDVAKA	300
Db	241	HVLLLSRSAIYLGRPDCGFEERVFSAYHSSLRAFTSLNCVADPILYCLVNNEGARSDVAKA	300
Qy	301	LHNLLRFLASDKPQEMANASLTLETPLTSKRNSTAKAMTGSWAATPPSEGDQVQLKMLPP	360
Db	301	LHNLLRFLASDKPQEMANASLTLETPLTSKRNSTAKAMTGSWAATPPSQGDQVQLKMLPP	360
Qy	361	AQ 362	
Db	361	AQ 362	